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Identification of drought tolerance candidate proteins and genes in reproductive stage of wheat

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Abstract

Reproductive development is the most water-stress-sensitive phase in the life of a cereal crop. We applied a proteomic approach to analysis the effects of drought stress on anther proteome and identification of candidate proteins and genes in drought tolerant, Dezful-10 and susceptible, Shiraz, wheat genotypes. Our results showed that short-term stresses at meiosis and mitosis stages declined plant seed setting and the meiosis stage is more sensitive to drought stress. Mass spectrometry analysis of responsive proteins revealed that several important protein in plant adaptation to drought stress are up-regulated only in tolerant plant including raftin, vacuolar invertase, putative PrMC3, Esterase/lipase, reversibly glycosylated polypeptide and subtilisin like serine protease. The expression of the selected proteins which were the representatives of the down-regulated proteins and of the up-regulated proteins in wheat genotypes were further assessed at the transcription level using real-time PCR.

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